

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/878,168DATE: 09/03/97
TIME: 12:58:39

INPUT SET: S20071.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Ashkenazi, Avi J.
6 Baker, Kevin
7 Gurney, Austin
8 Wood, William
9
10 (ii) TITLE OF INVENTION: Apo-2DcR
11
12 (iii) NUMBER OF SEQUENCES: 13
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: Genentech, Inc.
16 (B) STREET: 460 Point San Bruno Blvd
17 (C) CITY: South San Francisco
18 (D) STATE: California
19 (E) COUNTRY: USA
20 (F) ZIP: 94080
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: WinPatin (Genentech)
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER:
30 (B) FILING DATE: 18-Jun-1997
31 (C) CLASSIFICATION:
32
33 (viii) ATTORNEY/AGENT INFORMATION:
34 (A) NAME: Marschang, Diane L.
35 (B) REGISTRATION NUMBER: 35,600
36 (C) REFERENCE/DOCKET NUMBER: P1110
37
38 (ix) TELECOMMUNICATION INFORMATION:
39 (A) TELEPHONE: 415/225-5416
40 (B) TELEFAX: 415/952-9881
41 (C) TELEX: 910/371-7168
42
43 (2) INFORMATION FOR SEQ ID NO:1:
44
45 (i) SEQUENCE CHARACTERISTICS:
46 (A) LENGTH: 259 amino acids

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47      (B) TYPE: Amino Acid
48      (D) TOPOLOGY: Linear
49
50      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
51
52      Met Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile Val
53      1          5          10          15
54
55      Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg
56      20          25          30
57
58      Gln Glu Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg
59      35          40          45
60
61      His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly Ser His Arg Ser
62      50          55          60
63
64      Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
65      65          70          75
66
67      Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val
68      80          85          90
69
70      Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg
71      95          100          105
72
73      Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn
74      110          115          120
75
76      Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu
77      125          130          135
78
79      Val Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val
80      140          145          150
81
82      Glu Glu Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu
83      155          160          165
84
85      Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
86      170          175          180
87
88      Glu Thr Met Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
89      185          190          195
90
91      Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
92      200          205          210
93
94      Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu
95      215          220          225
96
97      Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Ser Ser His Tyr
98      230          235          240
99

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100 Leu Ser Cys Thr Ile Val Gly Ile Ile Val Leu Ile Val Leu Leu
101 245 250 255

102
103 Ile Val Phe Val
104 259

106 (2) INFORMATION FOR SEQ ID NO:2:

107
108 (i) SEQUENCE CHARACTERISTICS:
109 (A) LENGTH: 1180 base pairs
110 (B) TYPE: Nucleic Acid
111 (C) STRANDEDNESS: Single
112 (D) TOPOLOGY: Linear

114 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

115
116
117 GCTGTGGGAA CCTCTCCACG CGCACGAACT CAGCCAACGA TTTCTGATAG 50
118
119 ATTTTGGGGA GTTTGACCAG AGATGCAAGG GGTGAAGGAG CGCTTCCTAC 100
120
121 CGTTAGGGAA CTCTGGGGAC AGAGCGCCCC GGCCGCCTGA TGGCCGAGGC 150
122
123 AGGGTGCGAC CCAGGACCCA GGACGGCGTC GGGAACCATA CC ATG 195
124 Met
125 1
126
127 GCC CGG ATC CCC AAG ACC CTA AAG TTC GTC GTC GTC ATC 234
128 Ala Arg Ile Pro Lys Thr Leu Lys Phe Val Val Val Ile
129 5 10
130
131 GTC GCG GTC CTG CTG CCA GTC CTA GCT TAC TCT GCC ACC 273
132 Val Ala Val Leu Leu Pro Val Leu Ala Tyr Ser Ala Thr
133 15 20 25
134
135 ACT GCC CGG CAG GAG GAA GTT CCC CAG CAG ACA GTG GCC 312
136 Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala
137 30 35 40
138
139 CCA CAG CAA CAG AGG CAC AGC TTC AAG GGG GAG GAG TGT 351
140 Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys
141 45 50
142
143 CCA GCA GGA TCT CAT AGA TCA GAA CAT ACT GGA GCC TGT 390
144 Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala Cys
145 55 60 65
146
147 AAC CCG TGC ACA GAG GGT GTG GAT TAC ACC AAC GCT TCC 429
148 Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser
149 70 75
150
151 AAC AAT GAA CCT TCT TGC TTC CCA TGT ACA GTT TGT AAA 468
152 Asn Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys

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	80	85	90	
153				
154				
155	TCA GAT CAA AAA CAT AAA AGT TCC TGC ACC ATG ACC AGA			507
156	Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr Arg			
157	95	100		105
158				
159	GAC ACA GTG TGT CAG TGT AAA GAA GGC ACC TTC CGG AAT			546
160	Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn			
161	110	115		
162				
163	GAA AAC TCC CCA GAG ATG TGC CGG AAG TGT AGC AGG TGC			585
164	Glu Asn Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys			
165	120	125		130
166				
167	CCT AGT GGG GAA GTC CAA GTC AGT AAT TGT ACG TCC TGG			624
168	Pro Ser Gly Glu Val Gln Val Ser Asn Cys Thr Ser Trp			
169	135	140		
170				
171	GAT GAT ATC CAG TGT GTT GAA GAA TTT GGT GCC AAT GCC			663
172	Asp Asp Ile Gln Cys Val Glu Glu Phe Gly Ala Asn Ala			
173	145	150		155
174				
175	ACT GTG GAA ACC CCA GCT GCT GAA GAG ACA ATG AAC ACC			702
176	Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met Asn Thr			
177	160	165		170
178				
179	AGC CCG GGG ACT CCT GCC CCA GCT GCT GAA GAG ACA ATG			741
180	Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met			
181	175	180		
182				
183	AAC ACC AGC CCA GGG ACT CCT GCC CCA GCT GCT GAA GAG			780
184	Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu			
185	185	190		195
186				
187	ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA GCT GCT			819
188	Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala			
189	200	205		
190				
191	GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT GCC CCA			858
192	Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro Ala Pro			
193	210	215		220
194				
195	GCT GCT GAA GAG ACA ATG ACC ACC AGC CCG GGG ACT CCT			897
196	Ala Ala Glu Glu Thr Met Thr Thr Ser Pro Gly Thr Pro			
197	225	230		235
198				
199	GCC TCT TCT CAT TAC CTC TCA TGC ACC ATC GTA GGG ATC			936
200	Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile			
201	240	245		
202				
203	ATA GTT CTA ATT GTG CTT CTG ATT GTG TTT GTT T			970
204	Ile Val Leu Ile Val Leu Leu Ile Val Phe Val			
205	250	255		259

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206
207 GAAAGACTTC ACTGTGGAAG AAATTCCTTC CTTACCTGAA AGGTTTCAGGT 1020
208
209 AGGCGCTGGC TGAGGGCGGG GGGCGCTGGA CACTCTCTGC CCTGCCTCCC 1070
210
211 TCTGCTGTGT TCCCACAGAC AGAAACGCCT GCCCCTGCCC CAAAAAAAAA 1120
212
213 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1170
214
215 AAAAAAAAAA 1180
216

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

225
226 Met Gln Gln Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly
227 -40 -35 -30
228
229 Asp Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro
230 -25 -20 -15
231
232 Arg Thr Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro
233 -10 -5 1 5
234
235 Lys Thr Leu Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro
236 10 15 20
237
238 Val Leu Ala Tyr Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro
239 25 30 35
240
241 Gln Gln Thr Val Ala Pro Gln Gln Gln Arg His Ser Phe Lys Gly
242 40 45 50
243
244 Glu Glu Cys Pro Ala Gly Ser His Arg Ser Glu His Thr Gly Ala
245 55 60 65
246
247 Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr Thr Asn Ala Ser Asn
248 70 75 80
249
250 Asn Glu Pro Ser Cys Phe Pro Cys Thr Val Cys Lys Ser Asp Gln
251 85 90 95
252
253 Lys His Lys Ser Ser Cys Thr Met Thr Arg Asp Thr Val Cys Gln
254 100 105 110
255
256 Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn Ser Pro Glu Met Cys
257 115 120 125
258

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SEQUENCE VERIFICATION REPORT
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Error

Original Text